

## SEQUENCE LISTING

<110> Hua, Shao-bing  
 Pauling, Michelle H.  
 Zhu, Li

<120> HIGH THROUGHPUT GENERATION OF HUMAN MONOCLONAL ANTIBODY AGAINST PEPTIDE FRAGMENTS DERIVED FROM MEMBRANE PROTEINS

<130> 25636-717

<160> 54

<170> PatentIn version 3.1

<210> 1  
 <211> 352  
 <212> PRT  
 <213> Homo sapiens

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Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu  
 20 25 30

Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn  
 35 40 45

Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met  
 50 55 60

Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu  
 65 70 75 80

Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe  
 85 90 95

Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe  
 100 105 110

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Pro Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu  
115 120 125

Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe  
130 135 140

Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser  
145 150 155 160

Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr  
165 170 175

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn  
180 185 190

Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu  
195 200 205

Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys  
210 215 220

Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile  
225 230 235 240

Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu  
245 250 255

Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser  
260 265 270

Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr  
275 280 285

His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe  
290 295 300

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Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe  
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Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser  
325 330 335

Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu  
340 345 350

<210> 2  
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<400> 2

Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp  
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Gln

<210> 3  
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<400> 3

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Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr His Cys  
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<210> 4  
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Gly Gly Gly Ser  
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<400> 7

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<211> 36

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<213> Homo sapiens

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Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu  
20 25 30

Leu Pro Pro Leu  
35

<210> 9

<211> 32

<212> PRT

<213> Homo sapiens

<400> 9

Thr Arg Ser Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe  
1 5 10 15

Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn Phe Gln Thr Leu Lys Ile  
20 25 30

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<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Primer

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30

<210> 11

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 11

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31

<210> 12

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 12

ggagaattca ccagatctca aaaagaagg

29

<210> 13

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 13

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<210> 14

<211> 21

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<213> Artificial Sequence

<220>

<223> Primer

<400> 14

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<210> 15

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 15

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<210> 16

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<212> DNA

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<220>

<223> Clone 15.186.35

<400> 16

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120

agccccag gaaaggccct tgagtggctt gcaagcataa attggaatga tgataagtgc  
180

acagcccat ctctgaaaag caggctcacc atcaccaagg acacccccaa aaaccaggtg  
240

cccttgcaa tgagcaacat ggaccctgcg gacacagcca catattcctg tgcactcgat  
300

tgccccccc atgatagtgg cccgcaatct tttgatgctt ctgatgtctg gggcccaggg  
360

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acaatgggtca ccgtctcttc aggcgggtggt ggatcaggcg gcggaggatc tggcggaggt  
420

ggcagcgggtg gtggaggcag ttcctatgag ctgatgcagc taccctcagt gtccgtgtcc  
480

ccaggacaga cagccagcat cacctgctct ggagataatt tgggggataa atatgcctgc  
540

tggtatcaac agaagccagg ccggtcccct gtgctgggtca tttatggaga taacaagcgg  
600

ccctcaggga tccttgagcg attctctggc tccaactctg ggaacacagc cactctgacc  
660

atcagcggga ccaggctat ggatgaggct gactattact gtcaggcgtg ggacaccagc  
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<210> 17

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> Clone 15.186.35

<400> 17

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln  
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Ser Thr Ser  
20 25 30

Gly Val Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Ser Ile Asn Trp Asn Asp Asp Lys Cys Tyr Ser Pro Ser  
50 55 60



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Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Pro Lys Asn Gln Val
65                               70                               75                               80

Val Leu Ala Met Ser Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Ser
85                               90                               95

Cys Ala Leu Asp Met Pro Pro His Asp Ser Gly Pro Gln Ser Phe Asp
100                              105                              110

Ala Ser Asp Val Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser Gly
115                              120                              125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130                              135                              140

Gly Gly Ser Ser Tyr Glu Leu Met Gln Leu Pro Ser Val Ser Val Ser
145                              150                              155                              160

Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Asn Leu Gly Asp
165                              170                              175

Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Arg Ser Pro Val Leu
180                              185                              190

Val Ile Tyr Gly Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe
195                              200                              205

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
210                              215                              220

Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Thr Ser
225                              230                              235                              240

Thr Ala Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
245                              250

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<223> Clone 15.150.11

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120
ccaggggagg gactggagtg gattggtttc atcttcttcg atgggagcac caactacaac
180
ccctccctca acggctcgagt caccatctca ctcgacacgt cgaagaatca gctctccctg
240
aggctgacct ctgtgaccgc tgcggacacg gccgtgtatt tctgtgagag actaaagggg
300
gcgtgggttat tgtctgaacc cccttacttc agctccgacg gcatggacgt ctggggccaa
360
gggaccacgg tcaccgtccc ctcaggcggc ggtggatcag gcggcggagg atctggcgga
420
ggtggcagcg gtggtggagg cagtaatttt atgctgactc agccccctc agcgtctggg
480
acccccgggc agagggtcag catctcttgt tctgggagca gctccgacat cggaagtaat
540
actgtaaact ggtaccagca actcccagga acggccccca aactcctcat ctatagtaat
600
aatcagcggc cctcaggggt cctgaccga ttctctggct tcaagtctgg cacctcagcc
660
tccttgggtc tcagtggcct ccagtctgag gatgaggctg attattattg tgcagcatgg
720
gatgagagcc tgaatgggtg ggtgttcggc ggaggaccaa gg
762

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<210> 19  
 <211> 254  
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 <213> Artificial Sequence

<220>  
 <223> Clone 15.150.11

<400> 19

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Gly His Asp  
 20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp Ile  
 35 40 45

Gly Phe Ile Phe Phe Asp Gly Ser Thr Asn Tyr Asn Pro Ser Leu Asn  
 50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Leu Ser Leu  
 65 70 75 80

Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala  
 85 90 95

Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser  
 100 105 110

Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Pro Ser  
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
 130 135 140

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly

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145 150 155 160

Thr Pro Gly Gln Arg Val Ser Ile Ser Cys Ser Gly Ser Ser Ser Asp  
165 170 175

Ile Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala  
180 185 190

Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro  
195 200 205

Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser Leu Val Ile  
210 215 220

Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp  
225 230 235 240

Asp Glu Ser Leu Asn Gly Val Val Phe Gly Gly Gly Pro Arg  
245 250

<210> 20  
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<212> DNA  
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acctgcgctg tctctggtgc gtcgtttagt ggttattatt ggagctggat ccgccagccc  
120

ccagggaagg ggctggagtg gattggggag atcaatcatc gtggaagcac tacctacaac  
180

cgtccctcg acggtcgagt caccatatca ttagacacat ctaccaacca gatctccctt  
240

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aaactgacct ctatgaccgc cgcggacacg gccgtgtatt actgtgcgag gacagtggct  
300

ggtagtagtg actactgggg ccaggggaacc ctgggtcaccg tttcctcagg gagtgcattcc  
360

gccccaacgg gcggtgggtg atcaggcggc ggaggatctg gcggaggtgg cagcgggtgg  
420

ggaggcagta aaacgacact cacgcagtct ccagcattca tgtcagcgac tccaggagac  
480

aaagtcagca tctcctgcaa agccagccga gacgttgatg atgatgtgaa ctggtaccaa  
540

cagagaccag gagaagctcc tatttttcatt attgaagatg ctactactct cgttcctgga  
600

atctcacctc gattcagtgg cagcgggtat ggaaccgatt ttaccctcac aattaataac  
660

atcgattctg aggatgctgc atattatttc tgtctacaac atgataattt cccgctcacc  
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<212> PRT  
<213> Artificial Sequence

<220>  
<223> Clone 15.150.12

<400> 21

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Ser Trp Gly  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Ala Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

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Gly Glu Ile Asn His Arg Gly Ser Thr Thr Tyr Asn Pro Ser Leu Asp  
 50 55 60  
 Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Thr Asn Gln Ile Ser Leu  
 65 70 75 80  
 Lys Leu Thr Ser Met Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95  
 Arg Thr Val Ala Gly Thr Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val  
 100 105 110  
 Thr Val Ser Ser Gly Ser Ala Ser Ala Pro Thr Gly Gly Gly Gly Ser  
 115 120 125  
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys  
 130 135 140  
 Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly Asp  
 145 150 155 160  
 Lys Val Ser Ile Ser Cys Lys Ala Ser Arg Asp Val Asp Asp Asp Val  
 165 170 175  
 Asn Trp Tyr Gln Gln Arg Pro Gly Glu Ala Pro Ile Phe Ile Ile Glu  
 180 185 190  
 Asp Ala Thr Thr Leu Val Pro Gly Ile Ser Pro Arg Phe Ser Gly Ser  
 195 200 205  
 Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Asp Ser Glu  
 210 215 220  
 Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Asn Phe Pro Leu Thr  
 225 230 235 240

<sup>2</sup> Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
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<210> 22  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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 120  
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 180  
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 240  
 gtccttaciaa tgaccaacgt ggaccacagcg gacacagcca cctattactg tacacacgag  
 300  
 caatactatt atgatactag tggtcagcca tactactttg acttctgggg ccagggcacc  
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 420  
 agcggtggtg gaggcagtaa catccagggtg acccagtctc catcctccct gtctgcatct  
 480  
 gtaggagaca gagtcaccat gacttgccgg gcgagtcagg acattaggaa gaatttaa  
 540  
 tggatatcagc aaaaaccagg gaaagcccct aaggctctga tctacgatgc atccgatttg  
 600  
 gaaacaggga tcccatcaag gttcagtgga agtggatctg ggacagattt tatectcacc  
 660

atcagcagcc tgcagcctga agatattgca acatactact gtcaacagtc tgattattta  
720

ccgctcactt tcggcggagg gaccaaagtg gatatcaaa  
759

<210> 23  
<211> 253  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Clone 15.150.24

<400> 23

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln  
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Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Thr Thr  
20 25 30

Gly Glu Gly Val Gly Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Ser Pro Ser  
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Lys Gln Val  
65 70 75 80

Val Leu Thr Met Thr Asn Val Asp Pro Ala Asp Thr Ala Thr Tyr Tyr  
85 90 95

Cys Thr His Glu Gln Tyr Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr  
100 105 110

Phe Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly  
115 120 125



Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
130 135 140

Gly Ser Asn Ile Gln Val Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser  
145 150 155 160

Val Gly Asp Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asp Ile Arg  
165 170 175

Lys Asn Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val  
180 185 190

Leu Ile Tyr Asp Ala Ser Asp Leu Glu Thr Gly Ile Pro Ser Arg Phe  
195 200 205

Ser Gly Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu  
210 215 220

Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Tyr Leu  
225 230 235 240

Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys  
245 250

<210> 24

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Clone 15.186.35 Variant

<400> 24

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120

cagccccag gaaaggccct tgagtggctt gcaagcataa attggaatga tgataagtgc  
 180  
 tacagcccat ctctgaaaag caggctcacc atcaccaagg acacccccaa aaaccagggtg  
 240  
 gtccttgcaa tgagcaacat ggaccctgcg gacacagcca catattcctg tgcactcgat  
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 360  
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 480  
 ccaggacaga cagccagcat cacctgctct ggagataatt tgggggataa atatgcctgc  
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 660  
 atcagcggga cccaggctat ggatgaggct gactattact gtcaggcgtg ggacaccagc  
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 759

<210> 25  
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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Thr | Leu | Lys | Glu | Ser | Gly | Pro | Thr | Leu | Val | Lys | Pro | Thr | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

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Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Ser Thr Ser  
20 25 30

Gly Val Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Ser Ile Asn Trp Asn Asp Asp Lys Cys Tyr Ser Pro Ser  
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Pro Lys Asn Gln Val  
65 70 75 80

Val Leu Ala Met Ser Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Ser  
85 90 95

Cys Ala Leu Asp Met Pro Pro His Asp Ser Gly Pro Gln Ser Phe Asp  
100 105 110

Ala Ser Asp Val Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser Gly  
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
130 135 140

Gly Gly Ser Ser Tyr Glu Leu Met Gln Leu Pro Ser Val Ser Val Ser  
145 150 155 160

Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Asn Leu Gly Asp  
165 170 175

Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Arg Ser Pro Val Leu  
180 185 190

Val Ile Tyr Gly Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe  
195 200 205

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr  
210 215 220

Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Thr Ser  
225 230 235 240

Thr Ala Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu  
245 250

<210> 26

<211> 774

<212> DNA

<213> Artificial Sequence

<220>

<223> Clone 15.150.11 Variant

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120

ccaggggagg gactggagtg gattggtttc atcttcttcg atgggagcac caactacaac  
180

ccctccctca acggtcgagt caccatctca ctgcacacgt cgaagaatca gctctccctg  
240

aggctgacct ctgtgaccgc tgcggacacg gccgtgtatt tctgtgcgag actaaagggg  
300

gcgtgggttat tgtctgaacc cccttacttc agctccgacg gcatggacgt ctggggccaa  
360

gggaccacgg tcaccgtctc ctcaggcggc ggtggatcag gcggcggagg atctggcgga  
420

ggtggcagcg gtggtggagg cagtaatttt atgctgactc agccccctc agcgtctggg  
480

acccccgggc agagggtcag catctcttctg tctgggagca gctccgacat cggaagtaat  
540

actgtaaact ggtaccagca actcccagga acggccccca aactcctcat ctatagtaat  
600

aatcagcggc cctcaggggt ccctgaccga ttctctggct tcaagtctgg cacctcagcc  
660

tccctgggtca tcagtggcct ccagtctgag gatgaggctg attattattg tgcagcatgg  
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<210> 27

<211> 258

<212> PRT

<213> Artificial Sequence

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<223> Clone 15.150.11

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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Gly His Asp  
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp Ile  
35 40 45

Gly Phe Ile Phe Phe Asp Gly Ser Thr Asn Tyr Asn Pro Ser Leu Asn  
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Leu Ser Leu  
65 70 75 80

Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala  
85 90 95

Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser

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      100              105              110
#
Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
    115              120              125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    130              135              140

Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly
    145              150              155              160

Thr Pro Gly Gln Arg Val Ser Ile Ser Cys Ser Gly Ser Ser Ser Asp
    165              170              175

Ile Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala
    180              185              190

Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro
    195              200              205

Asp Arg Phe Ser Gly Phe Lys Ser Gly Thr Ser Ala Ser Leu Val Ile
    210              215              220

Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp
    225              230              235              240

Asp Glu Ser Leu Asn Gly Val Val Phe Gly Gly Gly Thr Lys Val Thr
    245              250              255

Val Leu

```

<210> 28  
 <211> 750  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Clone 15.150.12 Variant

<400> 28

caggtgcagc tacagcagtg gggcgcagga ctgttgaagt cttggggaac cctgtccctc  
60

acctgcgctg tctctggtgc gtcgtttagt ggttattatt ggagctggat ccgccagccc  
120

ccaggaagg ggctggagtg gattggggag atcaatcatc gtggaagcac tacctacaac  
180

ccgtccctcg acggtcgagt caccatatca ttagacacat ctaccaacca gatctccctt  
240

aaactgacct ctatgaccgc cgcggacacg gccgtgtatt actgtgagag gacagtggct  
300

ggtactagtg actactgggg ccaggaacc ctggtcaccg tttcctcagg gagtgcattc  
360

gccccaacgg gcggtggtgg atcaggcggc ggaggatctg gcggaggtgg cagcgggtgt  
420

ggaggcagtg aaacgacact cacgcagtct ccagcattca tgtcagcgac tccaggagac  
480

aaagtcagca tctcctgcaa agccagccga gacgttgatg atgatgtgaa ctggtaccaa  
540

cagagaccag gagaagctcc tattttcatt attgaagatg ctactactct cgttcctgga  
600

atctcacctc gattcagtgg cagcgggtat ggaaccgatt ttaccctcac aattaataac  
660

atcgattctg aggatgctgc atattatttc tgtctacaac atgataattt cccgctcacc  
720

ttcggcggag ggaccaaggt ggagatcaaa  
750

<210> 29

<211> 250

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Clone 15.150.12 Variant

&lt;400&gt; 29

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Ser Trp Gly  
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Ala Ser Phe Ser Gly Tyr  
 20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Asn His Arg Gly Ser Thr Thr Tyr Asn Pro Ser Leu Asp  
 50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Thr Asn Gln Ile Ser Leu  
 65 70 75 80

Lys Leu Thr Ser Met Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
 85 90 95

Arg Thr Val Ala Gly Thr Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val  
 100 105 110

Thr Val Ser Ser Gly Ser Ala Ser Ala Pro Thr Gly Gly Gly Gly Ser  
 115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu  
 130 135 140

Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly Asp  
 145 150 155 160

Lys Val Ser Ile Ser Cys Lys Ala Ser Arg Asp Val Asp Asp Asp Val  
 165 170 175



Asn Trp Tyr Gln Gln Arg Pro Gly Glu Ala Pro Ile Phe Ile Ile Glu  
180 185 190

Asp Ala Thr Thr Leu Val Pro Gly Ile Ser Pro Arg Phe Ser Gly Ser  
195 200 205

Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Asp Ser Glu  
210 215 220

Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Asn Phe Pro Leu Thr  
225 230 235 240

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
245 250

<210> 30

<211> 759

<212> DNA

<213> Artificial Sequence

<220>

<223> Clone 15.150.24 Variant

<400> 30

caggtcacct tgaaggagtc tggctctacg ctgggtgaaac ccacacagac cctcacgctg  
60

acctgcacct tctctggggtt ctcaactcaga actactggag aggggtgtggg ctgggtccgt  
120

cagccccag gaaaggccct ggaatggctt gcactcattt attgggatga tgataagcgc  
180

tacagcccat ctctgaagag caggctcacc atcaccaagg acacctccaa aaagcagggtg  
240

gtccttataa tgaccaacgt ggaccacagcg gacacagcca cctattactg tacacacgag  
300

caatactatt atgatactag tggtcagcca tactactttg acttctgggg ccagggcacc  
360

ctggtcaccg tctcctcagg cggtggtgga tcaggcggcg gaggatctgg cggaggtggc  
420

agcgggtggtg gaggcagtaa catccaggtg acccagtctc catcctccct gtctgcatct  
480

gtaggagaca gagtcaccat gacttgccgg gcgagtcagg acattaggaa gaatttaa  
540

tggtatcagc aaaaaccagg gaaagcccct aaggtcctga tctacgatgc atccgatttg  
600

gaaacagggg tcccatcaag gttcagtgga agtggatctg ggacagattt tatectcacc  
660

atcagcagcc tgcagcctga agatattgca acatactact gtcaacagtc tgattattta  
720

ccgctcactt tcggcggagg gaccaaagtg gatatcaaa  
759

<210> 31

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> Clone 15.150.24 Variant

<400> 31

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln  
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Thr Thr  
20 25 30

Gly Glu Gly Val Gly Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu  
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Ser Pro Ser  
50 55 60

65 Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Lys Gln Val  
 70 75 80  
 Val Leu Thr Met Thr Asn Val Asp Pro Ala Asp Thr Ala Thr Tyr Tyr  
 85 90 95  
 Cys Thr His Glu Gln Tyr Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr  
 100 105 110  
 Phe Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly  
 115 120 125  
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
 130 135 140  
 Gly Ser Asn Ile Gln Val Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser  
 145 150 155 160  
 Val Gly Asp Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asp Ile Arg  
 165 170 175  
 Lys Asn Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val  
 180 185 190  
 Leu Ile Tyr Asp Ala Ser Asp Leu Glu Thr Gly Ile Pro Ser Arg Phe  
 195 200 205  
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu  
 210 215 220  
 Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Tyr Leu  
 225 230 235 240  
 Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys  
 245 250

<210> 32  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> VH CDR2

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = Asparagine or Threonine

<400> 32  
 Gly Ser Thr Xaa Tyr Asn Pro Ser Leu  
 1 5

<210> 33  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> VL CDR2

<220>  
 <221> MISC\_FEATURE  
 <222> (3)..(4)  
 <223> X3 = Asparagine or Threonine  
 X4 = Threonine or Aspartic acid

<400> 33

Asp Ala Xaa Xaa Leu  
 1 5

<210> 34  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

<400> 34

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Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1      5      10      15

Thr Leu Thr Leu Thr Cys Thr Leu Ser Gly Phe Ser Leu Ser Thr Ser
      20      25      30

Gly Val Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
      35      40      45

Trp Leu Ala Ser Ile Asn Trp Asn Asp Asp Lys Cys Tyr Ser Pro Ser
50      55      60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Pro Lys Asn Gln Val
65      70      75      80

Val Leu Ala Met Ser Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Ser
      85      90      95

Cys Ala Leu Asp Met Pro Pro His Asp Ser Gly Pro Gln Ser Phe Asp
      100      105      110

Ala Ser Asp Val Trp Gly Pro Gly Thr Met Val Thr Val Ser Ser
      115      120      125

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<210> 35
<211> 106
<212> PRT
<213> Homo sapiens

<400> 35

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Ser Tyr Glu Leu Met Gln Leu Pro Ser Val Ser Val Ser Pro Gly Gln
1      5      10      15

Thr Ala Ser Ile Thr Cys Ser Gly Asp Asn Leu Gly Asp Lys Tyr Ala
      20      25      30

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Genetastix.717.ST25

Cys Trp Tyr Gln Gln Lys Pro Gly Arg Ser Pro Val Leu Val Ile Tyr  
35 40 45

Gly Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser  
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met  
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Thr Ser Thr Ala Val  
85 90 95

Phe Gly Thr Gly Thr Lys Leu Thr Val Leu  
100 105

<210> 36  
<211> 126  
<212> PRT  
<213> Homo sapiens  
<400> 36

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Gly His Asp  
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp Ile  
35 40 45

Gly Phe Ile Phe Phe Asp Gly Ser Thr Asn Tyr Asn Pro Ser Leu Asn  
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Lys Asn Gln Leu Ser Leu  
65 70 75 80

Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala

Genetastix.717.ST25

85

90

95

Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser  
100 105 110

Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val  
115 120 125

<210> 37  
<211> 104  
<212> PRT  
<213> Homo sapiens

<400> 37

Asn Phe Met Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln  
1 5 10 15

Arg Val Ser Ile Ser Cys Ser Gly Ser Ser Ser Asp Ile Gly Ser Asn  
20 25 30

Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu  
35 40 45

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser  
50 55 60

Gly Phe Lys Ser Gly Thr Ser Ala Ser Leu Val Ile Ser Gly Leu Gln  
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Glu Ser Leu  
85 90 95

Asn Gly Val Val Phe Gly Gly Gly  
100

<210> 38  
<211> 116

Genetastix.717.ST25

<212> PRT

<213> Homo sapiens

<400> 38

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Ser Trp Gly  
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Ala Ser Phe Ser Gly Tyr  
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asn His Arg Gly Ser Thr Thr Tyr Asn Pro Ser Leu Asp  
50 55 60

Gly Arg Val Thr Ile Ser Leu Asp Thr Ser Thr Asn Gln Ile Ser Leu  
65 70 75 80

Lys Leu Thr Ser Met Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Thr Val Ala Gly Thr Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ser  
115

<210> 39

<211> 106

<212> PRT

<213> Homo sapiens

<400> 39

Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly Asp  
1 5 10 15



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Lys Val Ser Ile Ser Cys Lys Ala Ser Arg Asp Val Asp Asp Asp Val
      20                      25                      30

Asn Trp Tyr Gln Gln Arg Pro Gly Glu Ala Pro Ile Phe Ile Ile Glu
      35                      40                      45

Asp Ala Thr Thr Leu Val Pro Gly Ile Ser Pro Arg Phe Ser Gly Ser
      50                      55                      60

Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Asp Ser Glu
      65                      70                      75                      80

Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Asn Phe Pro Leu Thr
      85                      90                      95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
      100                      105

<210> 40
<211> 126
<212> PRT
<213> Homo sapiens

<400> 40

Gln Val Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1                      5                      10                      15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Arg Thr Thr
      20                      25                      30

Gly Glu Gly Val Gly Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu
      35                      40                      45

Trp Leu Ala Leu Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Ser Pro Ser
      50                      55                      60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Lys Gln Val

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Genetastix.717.ST25

65

70

75

80

Val Leu Thr Met Thr Asn Val Asp Pro Ala Asp Thr Ala Thr Tyr Tyr  
85 90 95

Cys Thr His Glu Gln Tyr Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr  
100 105 110

Phe Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120 125

<210> 41

<211> 107

<212> PRT

<213> Homo sapiens

<400> 41

Asn Ile Gln Val Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Met Thr Cys Arg Ala Ser Gln Asp Ile Arg Lys Asn  
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile  
35 40 45

Tyr Asp Ala Ser Asp Leu Glu Thr Gly Ile Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Ile Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Tyr Leu Pro Leu  
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys  
100 105

<210> 42  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Linker Sequence

<400> 42

Gly Gly Gly Gly Ser  
 1 5

<210> 43  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens  
 <400> 43

Arg Leu Lys Gly Ala Trp Leu Leu Ser Glu Pro Pro Tyr Phe Ser Ser  
 1 5 10 15

Asp Gly Met Asp Val  
 20

<210> 44  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 44

Arg Thr Val Ala Gly Thr Ser Asp Tyr  
 1 5

<210> 45  
 <211> 17  
 <212> PRT  
 <213> Homo sapiens

<400> 45

His Glu Gln Tyr Tyr Tyr Asp Thr Ser Gly Gln Pro Tyr Tyr Phe Asp  
 1 5 10 15

Phe

<210> 46  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens

<400> 46

Ala Ala Trp Asp Glu Ser Leu Asn Gly Val Val  
 1 5 10

<210> 47  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 47

Leu Gln His Asp Asn Phe Pro Leu Thr  
 1 5

<210> 48  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 48

Gln Gln Ser Asp Tyr Leu Pro Leu Thr  
 1 5

<210> 49  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Primer

<400> 49

ggagaattcg attatcaagt gtcaagtcca  
30

<210> 50

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 50

cgcggtatcct tagagcggag gcaggaggcg g  
31

<210> 51

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 51

ggagaattca ccagatctca aaaagaagg  
29

<210> 52

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 52

cgcggtatcct tatatcttta atgtctggaa att  
33

<210> 53

<211> 21

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 53  
caggaattct ttggcctgaa t  
21

<210> 54  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 54  
cgcggtatcct cagcagtgcg tcatccaag a  
31